RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/661,399
Source: IFW0
Date Processed by STIC: 11/5/04

ENTERED

IFWO

RAW SEQUENCE LISTING DATE: 11/05/2004
PATENT APPLICATION: **US/10/661,399** TIME: 12:27:17

Input Set : **A:\1200029-US2.ST25.txt**
Output Set: **N:\CRF4\11052004\J661399.raw**

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      3 <110> APPLICANT: Soll, Dieter
      5 <120> TITLE OF INVENTION: GlutRNAGLN AMIDOTRANSFERASE - A NOVEL ESSENTIAL
TRANSLATIONAL
      6       COMPONENT
      8 <130> FILE REFERENCE: 03818/1200029-US2
     10 <140> CURRENT APPLICATION NUMBER: 10/661,399
     11 <141> CURRENT FILING DATE: 2003-09-12
     13 <150> PRIOR APPLICATION NUMBER: 60/037,275
     14 <151> PRIOR FILING DATE: 1997-02-03
     16 <150> PRIOR APPLICATION NUMBER: PCT/US98/01860
     17 <151> PRIOR FILING DATE: 1998-02-03
     19 <150> PRIOR APPLICATION NUMBER: 09/355,622
     20 <151> PRIOR FILING DATE: 1999-09-23
     22 <160> NUMBER OF SEQ ID NOS: 8
     24 <170> SOFTWARE: PatentIn version 3.2
     26 <210> SEQ ID NO: 1
     27 <211> LENGTH: 3495
     28 <212> TYPE: DNA
     29 <213> ORGANISM: Bacillus subtilis
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     33 <221> NAME/KEY: misc_feature
     34 <222> LOCATION: (2330)..(2330)
     35 <223> OTHER INFORMATION: n is a, c, g, or t
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     39 <222> LOCATION: (2365)..(2365)
     40 <223> OTHER INFORMATION: n is a, c, g, or t
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     47 gaagaagtaa agcacgttgc gcaccttgca agacttgcga ttactgaaga agaagcaaaa    180
     49 atgttcactg aacagctcga cagtatcatt tcatttgccg aggagcttaa tgaggttaac    240
     51 acagacaatg tggagcctac aactcacgtg ctgaaaatga aaaatgtcat gagagaagat    300
     53 gaagcgggta aaggtcttcc ggttgaggat gtcatgaaaa atgcgcctga ccataaagac    360
     55 ggctatattc gtgtgccatc aattctggac taaaggaggg acacaagaat gtcattattt    420
     57 gatcataaaa tcacagaatt aaaacagctc atacataaaa aagagattaa gatttctgat    480
     59 ctggttgatg aatcttataa acgcatccaa gcggttgatg ataaggtaca agccttttg     540
     61 gcattagatg aagaaagagc gcgcgcatac gcgaaggagc ttgatgaggc ggttgacggc    600
     63 cgttctgagc acggtcttct tttcggtatg cccatcggcg taaaagataa tatcgtaaca    660
     65 aaagggctgc gcacaacatg ctccagcaaa attctcgaaa actttgatcc gatttacgat    720
     67 gctactgtcg ttcagcgcct tcaagacgct gaagcggtca caatcggaaa actgaacatg    780
     69 gacgaattcg ccatggggtc atctacagaa aactcagctt acaagctgac gaaaaaccct    840
     71 tggaacctgg atacagttcc cggcggttca agcggcggat ctgcagctgc ggttgctgcg    900
     73 ggagaagttc cgttttctct tggatctgac acaggcggct ccatccgtca gccggcatct    960
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(pg. 6)

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 77 gcatttgcgt cttcattgga ccaaatcgga ccgattacac gtacggttga ggataacgcg   1080
 79 tttttacttc aagcgatttc cggcgtagac aaaatggact ctacgagtgc aaatgtggac   1140
 81 gtgcctgatt ttctttcttc attaactggc gacatcaaag gactgaaaat cgccgttccg   1200
 83 aaagaatacc ttggtgaagg tgtcggcaaa gaagcgagag aatctgtctt ggcagcgctg   1260
 85 aaagtccttg aaggtctcgg cgctacatgg gaagaagtgt ctcttccgca cagtaaatac   1320
 87 gcgcttgcga catattacct gctgtcatct tctgaagcgt cagcgaacct tgcacgcttt   1380
 89 gacggcatcc gctacggcta ccgcacagac aacgcggata acctgatcga cctttacaag   1440
 91 caaacgcgcg ctgaaggttt cggaaatgaa gtcaaacgcc gcatcatgct cggaacgttt   1500
 93 gctttaagct caggctacta cgatgcgtac tacaaaaaag cgcaaaaagt gcgtacgttg   1560
 95 attaagaagg atttcgagga cgtatttgaa aaatatgatg ttattgttgg accgactaca   1620
 97 ccgacacctg cgtttaaaat cggtgaaaac acgaaggatc cgctcacaat gtacgcaaac   1680
 99 gatatcttaa cgattccggt caaccttgcg gcgtaccggg aatcaggtgc catgcggtta   1740
101 gcagacggac ttccgctcgg cctgcaaatc atcggaaaac actttgatga agcactgtat   1800
103 accgcgttgc tcatgcattt gaacaagcaa cagaccatca taaagcaaaa cctgaactgt   1860
105 aaggggtgaa aagaattgaa ctttgaaacg gtaatcggac ttgaagtcca cgttgagtta   1920
107 aaaacaaaat caaaaatttt ctcaagctct ccaacgccat tcggcgcgga ggcgaatacg   1980
109 cagacaagcg ttattgacct cggatatccg ggcgtcctgc ctgttctgaa caaagaagcc   2040
111 gttgaattcg caatgaaagc cgctatggcg ctcaactgtg agatcgcaac ggatacgaag   2100
113 tttgaccgca aaaactattt ctatcctgac aacccgaaag cgtatcagat ttctcaattt   2160
115 gataagccaa tcggcgaaaa cggctggatc gaaattgaag tcggcggcaa aacaaaacgc   2220
117 atcggcatca cgcgccttca tcttgaagag gatgccggaa aactgacgca tacgggcgac   2280
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123 caatatacag gcgtttctga ctgtaaaatg gaagaaggct cacttcgctg tgacgccaat   2460
125 atctctcttc gtccgatcgg ccaagaggaa ttcggcacaa aaacagaatt gaaaaacttg   2520
127 aactcctttg cgtttgttca aaaaggcctt gagcatgaag aaaaacgcca ggagcaggtt   2580
129 cttctttccg gcttcttcat ccagcaagaa actcgccgtt atgatgaagc aacgaagaaa   2640
131 accattctta tgcgtgtcaa agagggatct gacgactacc gttactttcc agagccagat   2700
133 ctagtcgagc tctacattga tgatgaatgg aaggaacgcg taaaagcaag cattcctgag   2760
135 cttccggatg agcgccgcaa gcgttatatc gaagagcttg gcttcgctgc atatgacgca   2820
137 atggttctga cgctgacaaa agaaatggct gatttcttcg aagaaaccgt tcaaaaaggc   2880
139 gctgaagcta aacaagcgtc taactggctg atgggtgaag tgtcagctta cctaaacgca   2940
141 gaacaaaaag agcttgccga tgttgccctg acacctgaag gccttgccgg catgatcaaa   3000
143 ttgattgaaa aaggaaccat ttcttctaag atcgcgaaga aagtgtttaa agaattgatt   3060
145 gaaaaaggcg gcgacgctga gaagattgtg aaagagaaag gccttgttca gatttctgac   3120
147 gaaggcgtgc ttctgaagct tgtcactgag gcgcttgaca acaatcctca atcaatcgaa   3180
149 gactttaaaa acggaaaaga ccgcgcgatc ggcttcctag tcggacagat tatgaaagcg   3240
151 tccaaaggac aagccaaccc gccgatggtc aacaaaattc tgcttgaaga aattaaaaaa   3300
153 cgctaataaa aaagcagccc ttagaggctg ctttttttat ggtcaaattg agataaagac   3360
155 aagatgaggg cccgaagcct ttcaacttct ttgtcgttgg ttccggccaa attggacagc   3420
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163 <211> LENGTH: 1155
164 <212> TYPE: PRT
165 <213> ORGANISM: Bacillus subtilis
168 <220> FEATURE:
169 <221> NAME/KEY: misc_feature
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Input Set : **A:\1200029-US2.ST25.txt**
Output Set: **N:\CRF4\11052004\J661399.raw**

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171 <223> OTHER INFORMATION: Xaa is Phe, Ser, Tyr, or Cys
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176 <223> OTHER INFORMATION: Xaa is Ser, Pro, Thr, or Ala
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185             20                  25                  30
188 His Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His Leu
189         35                  40                  45
192 Ala Arg Leu Ala Ile Thr Glu Glu Glu Ala Lys Met Phe Thr Glu Gln
193     50                  55                  60
196 Leu Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr
197 65                  70                  75                  80
200 Asp Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met
201                 85                  90                  95
204 Arg Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys
205             100                 105                 110
208 Asn Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu
209         115                 120                 125
212 Asp Arg Arg Asp Thr Arg Met Ser Leu Phe Asp His Lys Ile Thr Glu
213     130                 135                 140
216 Leu Lys Gln Leu Ile His Lys Lys Glu Ile Lys Ile Ser Asp Leu Val
217 145                 150                 155                 160
220 Asp Glu Ser Tyr Lys Arg Ile Gln Ala Val Asp Asp Lys Val Gln Ala
221                 165                 170                 175
224 Phe Leu Ala Leu Asp Glu Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu
225             180                 185                 190
228 Asp Glu Ala Val Asp Gly Arg Ser Glu His Gly Leu Leu Phe Gly Met
229         195                 200                 205
232 Pro Ile Gly Val Lys Asp Asn Ile Val Thr Lys Gly Leu Arg Thr Thr
233     210                 215                 220
236 Cys Ser Ser Lys Ile Leu Glu Asn Phe Asp Pro Ile Tyr Asp Ala Thr
237 225                 230                 235                 240
240 Val Val Gln Arg Leu Gln Asp Ala Glu Ala Val Thr Ile Gly Lys Leu
241                 245                 250                 255
244 Asn Met Asp Glu Phe Ala Met Gly Ser Ser Thr Glu Asn Ser Ala Tyr
245             260                 265                 270
248 Lys Leu Thr Lys Asn Pro Trp Asn Leu Asp Thr Val Pro Gly Gly Ser
249         275                 280                 285
252 Ser Gly Gly Ser Ala Ala Ala Val Ala Ala Gly Glu Val Pro Phe Ser
253     290                 295                 300
256 Leu Gly Ser Asp Thr Gly Gly Ser Ile Arg Gln Pro Ala Ser Phe Cys
257 305                 310                 315                 320
260 Gly Val Val Gly Leu Lys Pro Thr Tyr Gly Arg Val Ser Arg Tyr Gly
261                 325                 330                 335
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265             340                 345                 350
268 Thr Val Glu Asp Asn Ala Phe Leu Leu Gln Ala Ile Ser Gly Val Asp
269         355                 360                 365
272 Lys Met Asp Ser Thr Ser Ala Asn Val Asp Val Pro Asp Phe Leu Ser
273     370                 375                 380
276 Ser Leu Thr Gly Asp Ile Lys Gly Leu Lys Ile Ala Val Pro Lys Glu
277 385                 390                 395                 400
280 Tyr Leu Gly Glu Gly Val Gly Lys Glu Ala Arg Glu Ser Val Leu Ala
281                 405                 410                 415
284 Ala Leu Lys Val Leu Glu Gly Leu Gly Ala Thr Trp Glu Glu Val Ser
285             420                 425                 430
288 Leu Pro His Ser Lys Tyr Ala Leu Ala Thr Tyr Tyr Leu Leu Ser Ser
289         435                 440                 445
292 Ser Glu Ala Ser Ala Asn Leu Ala Arg Phe Asp Gly Ile Arg Tyr Gly
293     450                 455                 460
296 Tyr Arg Thr Asp Asn Ala Asp Asn Leu Ile Asp Leu Tyr Lys Gln Thr
297 465                 470                 475                 480
300 Arg Ala Glu Gly Phe Gly Asn Glu Val Lys Arg Arg Ile Met Leu Gly
301                 485                 490                 495
304 Thr Phe Ala Leu Ser Ser Gly Tyr Tyr Asp Ala Tyr Tyr Lys Lys Ala
305             500                 505                 510
308 Gln Lys Val Arg Thr Leu Ile Lys Lys Asp Phe Glu Asp Val Phe Glu
309         515                 520                 525
312 Lys Tyr Asp Val Ile Val Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys
313     530                 535                 540
316 Ile Gly Glu Asn Thr Lys Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile
317 545                 550                 555                 560
320 Leu Thr Ile Pro Val Asn Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met
321                 565                 570                 575
324 Arg Leu Ala Asp Gly Leu Pro Leu Gly Leu Gln Ile Ile Gly Lys His
325             580                 585                 590
328 Phe Asp Glu Ala Leu Tyr Thr Ala Leu Leu Met His Leu Asn Lys Gln
329         595                 600                 605
332 Gln Thr Ile Ile Lys Gln Asn Leu Asn Cys Lys Gly Lys Glu Leu Asn
333     610                 615                 620
336 Phe Glu Thr Val Ile Gly Leu Glu Val His Val Glu Leu Lys Thr Lys
337 625                 630                 635                 640
340 Ser Lys Ile Phe Ser Ser Ser Pro Thr Pro Phe Gly Ala Glu Ala Asn
341                 645                 650                 655
344 Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro Gly Val Leu Pro Val
345             660                 665                 670
348 Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys Ala Ala Met Ala Leu
349         675                 680                 685
352 Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp Arg Lys Asn Tyr Phe
353     690                 695                 700
356 Tyr Pro Asp Asn Pro Lys Ala Tyr Gln Ile Ser Gln Phe Asp Lys Pro
357 705                 710                 715                 720
360 Ile Gly Glu Asn Gly Trp Ile Glu Ile Glu Val Gly Gly Lys Thr Lys
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Input Set : **A:\1200029-US2.ST25.txt**
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     361                 725                 730                 735
     364 Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu Asp Ala Gly Lys Leu
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     369         755                 760                 765
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     373     770                 775                 780
     376 Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser Ile Ile Gln Tyr Thr
     377 785                 790                 795                 800
     380 Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser Leu Arg Cys Asp Ala
     381                 805                 810                 815
     384 Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr Lys Thr
     385             820                 825                 830
     388 Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val Gln Lys Gly Leu Glu
     389         835                 840                 845
     392 His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu Ser Gly Phe Phe Ile
     393     850                 855                 860
     396 Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr Ile Leu
     397 865                 870                 875                 880
     400 Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro Glu Pro
     401                 885                 890                 895
     404 Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg Val Lys
     405             900                 905                 910
     408 Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr Ile Glu
     409         915                 920                 925
     412 Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu Thr Lys
     413     930                 935                 940
     416 Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala Glu Ala
     417 945                 950                 955                 960
     420 Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr Leu Asn
     421                 965                 970                 975
     424 Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu Gly Leu
     425             980                 985                 990
     428 Ala Gly Met Ile Lys Leu Ile Glu  Lys Gly Thr Ile Ser  Ser Lys Ile
     429         995                 1000                1005
     432 Ala Lys  Lys Val Phe Lys Glu  Leu Ile Glu Lys Gly  Gly Asp Ala
     433     1010                1015                1020
     436 Glu Lys  Ile Val Lys Glu Lys  Gly Leu Val Gln Ile  Ser Asp Glu
     437     1025                1030                1035
     440 Gly Val  Leu Leu Lys Leu Val  Thr Glu Ala Leu Asp  Asn Asn Pro
     441     1040                1045                1050
     444 Gln Ser  Ile Glu Asp Phe Lys  Asn Gly Lys Asp Arg  Ala Ile Gly
     445     1055                1060                1065
     448 Phe Leu  Val Gly Gln Ile Met  Lys Ala Ser Lys Gly  Gln Ala Asn
     449     1070                1075                1080
     452 Pro Pro  Met Val Asn Lys Ile  Leu Leu Glu Glu Ile  Lys Lys Arg
     453     1085                1090                1095
     456 Lys Ser  Ser Pro Arg Leu Leu  Phe Leu Trp Ser Asn  Asp Lys Asp
     457     1100                1105                1110
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2330,2365
Seq#:2; Xaa Pos. 774,786
Seq#:5; N Pos. 455,490
Seq#:5; Xaa Pos. 152,164
Seq#:6; Xaa Pos. 152,164

VERIFICATION SUMMARY DATE: 11/05/2004
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L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2280
M:341 Repeated in SeqNo=1
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:768
M:341 Repeated in SeqNo=2
L:802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:432
M:341 Repeated in SeqNo=5
L:940 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:144
M:341 Repeated in SeqNo=6